



OIKE

## RAW SEQUENCE LISTING

DATE: 02/12/2002

PATENT APPLICATION: US/09/942,429A

TIME: 10:51:33

Input Set : A:\W122217.txt

Output Set: N:\CRF3\02122002\I942429A.raw

3 <110> APPLICANT: JORGE H. CAPDEVILA, MICHAEL WATERMAN, AND VIJAKUMAR HOLLA  
 5 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO  
 6 HYPERTENSION  
 8 <130> FILE REFERENCE: 22000.0110U2  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/942,429A  
 C--> 10 <141> CURRENT FILING DATE: 2000-08-29  
 10 <150> PRIOR APPLICATION NUMBER: 60/228,947  
 11 <151> PRIOR FILING DATE: 2000-08-29  
 13 <160> NUMBER OF SEQ ID NOS: 9  
 15 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 4123  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Artificial Sequence  
 22 <220> FEATURE:  
 23 <223> OTHER INFORMATION: Description of Artificial Sequence; Note =  
 24 synthetic construct  
 26 <221> NAME/KEY: misc\_feature  
 27 <222> LOCATION: (1)...(4123)  
 28 <223> OTHER INFORMATION: n = g, a, c or t(u)  
 30 <400> SEQUENCE: 1  
 31 gaattccact ctgaaagtgg gagaggatcc aagtagggaa ggagaaaggg tacaaaatga 60  
 32 cctgtcccaa gaaatggact ggatctttca atcattttact catccaacaa atatttgaag 120  
 33 ttgtaaaatg accacaaagt gggctaaaag ttcagacgta tggagcatgt cctctcgggt 180  
 34 ctttggtttt gaccaaagct cagaattgtg gaaagaaaga aaaagtagtg gggtatgcat 240  
 35 gttgtgtcac agtgaagat gaagtagtgg gtgttaaaga aaatgttttg atagataaag 300  
 36 gatcaagtga gcggcaaaca cacattcctg gcagagtga tgggctggct ttctagagat 360  
 37 tcttggttaa ataccttttg tgtttgcctc tttgtggtct tcacaactag gattaattta 420  
 38 gggaagataa tcatgatcca ggtgaggata aagattccag agaaaggctt atttctaccc 480  
 39 cttaacttct ttgtttttct tcctttctaa aagttttgtc atttttaaaa tttatttttt 540  
 40 atttaatttt ttcatgcaa tataatttga tcatattott tccttcctcc aactttctct 600  
 41 agatcctcag ggccttccta gctatccatc ttcattgtta tggatagact gacaaccaaa 660  
 42 acattctttc tctgcttaaa taatatctcc ataaaatcta taaataaatg aggtagtgtg 720  
 43 aaactatctc agcacttttc aattgattgg ctagtaatcc ttcaatatct catttttttt 780  
 44 aactttcgct ttatctattc tgtgtgnaca ttaatttttt tcaggcaagg cataatatat 840  
 45 atataattgg actgatttct ttattagagt ttgcctatg tgaggccaag aaatattctt 900  
 46 aaattaatga gtgactgaat aagtgtatgg caatttaagt atttagaaaa gaaaggtttt 960  
 47 attattccat tcagtcgaaga tagtgagaca gagaaagagt ctgtcacagg ctgtgtatgt 1020  
 48 ggtgaggctg attgagtctt gagccacctg aatgcaactg cactgttcca cctgctggca 1080  
 49 catccatcct ggatcaatct ggagtgtgac tgtgacaagt ctcagataaa atggaagaaa 1140  
 50 cagctggatt tggagtccag atgcaaagat gactataggt agaaactttc agcaattaca 1200  
 51 ttcatctgaa cacaccaact actgttgta tcatctcacc ctgaaattag gaaaatagta 1260  
 52 caagcagcta cacctattac atgtttggta aattagaatg tgaatttctt aatatccagg 1320

ENTERED

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53 ttaatgtota gtccatgact ttacctcacc agcaaggata tacataacat gcaatatgtg 1380
54 ctcaataaat agttgtgagt agttcagaga aatgggaatt ggtatacata tagatgttac 1440
55 caagactaga tactagagat ttgtttttac tgtttaccac agctgatgtt gcagattaat 1500
56 aaacttttga ttctgaggtc agtctctgtc tgtctctctc attccccctc ccacaagtag 1560
57 gtgtgtctac cttctcatga cttaaatgcg ggtttctaaa catttagtga cactagtgtat 1620
58 ccagaaacta ctaaccatgg gttttttttt atttagccct acaaggtaact tggatgggat 1680
59 ctctgggttc ttccaatggg ccttcttctc cagtctatct ctgggtgctg tcaaggcagt 1740
60 ccaattctac ttacgaaggc agtggtctgt caagaccctc cagcatttcc catgcatgcc 1800
61 ttccccactgg ctttgggggc accatctgaa gggacaagga gctccagcag attcttatat 1860
62 gggtagagaa attcccaagt gcctgcttac agtctctctc ggggagcaat atacgagtc 1920
63 tgccttatga tctgactat gtgaagggtg ttctggggag atcagatcca aaggcttctg 1980
64 gaatttatca attctttgct ccttggtatt gttatgggtt gctcctgttg aatgggaaga 2040
65 agtgggtcca gcacggcggt atgttgactc cagccttcca ctatgacatc ctcaaaccct 2100
66 atgtcaaaat catggcggac tctgtcaata taatgctaga taaatgggag aagcttgatg 2160
67 gccaggacca cctctgggag atcttccact gtgtttcatt gatgacactg gacactgtta 2220
68 tgaagtgtgc ttacagctac caaggcagtg ttcagttgga tgaaaattcc aagttgtata 2280
69 ctaaggctgt cgaggatcta aacaacctga ctttctttcg cctgcggaat gccttttata 2340
70 agtacaacat catctacaat atgtcctctg atggacgttt gtcccaccat gcctgccaga 2400
71 ttgctcacga gcacacagat ggagtgatca agatgaggaa gtctcagctg cagaatgagg 2460
72 aagagctgca gaaggccagg aagaagagac acttggtatt cttggacatc ctcttgtttg 2520
73 ccagaatgga ggataggaac agcttgtctg atgaggacct gcgtgcagag gtggacacat 2580
74 tcatgtttga gggtcattgac actacagcca gtggaatttc ctggatttcc tatgctctgg 2640
75 ccaccacccc tgagcaccac cagagatgca gagaggagt gcagagcatt ctgggtgatg 2700
76 gaacctctgt cactgtggac catctggggc agatgcccta caccaccatg tgcataagg 2760
77 aggccctgag gctctatcca ccagtaatat ctgtgagctg agagctcagc tcacctgtca 2820
78 cttcccaga tggacgtctc ataccaaaag gtatcacagc cacaatttcc atttatggcc 2880
79 tacatcataa cccacgtttc tggccaaacc caaagtggtt tgaccctctc agatttgcac 2940
80 cagattcttc tcaccatagc catgcttacc tgccattctc aggaggatca aggaactgca 3000
81 ttgggaaaca gtttgcctat aacgagctga aggtggctgt ggccctgacc ctgcttgcct 3060
82 ttgaattgct gccagatccc accaggatcc cagtcccat tgcaagactt gtgttgaagt 3120
83 ccaagaatgg gatccacctg tgtctcaaga agctaagata attctgatgg agtcagggca 3180
84 gctccagagg tctgtgcctt gcaataacct cttttgtctc tggcttttct gtactttgct 3240
85 ttctctttga ttcccattct tctgtctctc gcaatgtgtc ctgtcatctc atctttctgc 3300
86 cctcatttct gtagcttttc ctctagacac ctctctaacc tgtgcatgta cctgtttccc 3360
87 atctcgtctt aactctgacc agccactgaa cctgcagcca gcagcctgtc cccagcctg 3420
88 ttcaccctc ataaccattg cactgacaga ggaagatata ttttagagg agacacttgt 3480
89 acctttctct ccttccagtt attagactct tgggacaatg gacatcatga attaaaacgt 3540
90 tcttagaaat cacatgctgg gagaaaatta aactaaaat ctggtaccag ccagaggaag 3600
91 gaacttgact caaaataaga gattttttaga tatttctgtc tgtctcatag ttaaaattaa 3660
92 tgttttctct ctttctggca tatgctcat ctttctatg aagtagtaat actgatacag 3720
93 aaaggtagag agaaatgaat agtttttctc actttgggac aaactgtgaa aaaatccatt 3780
94 ttatttctac aatttctgtt tcccaatttc atttaagaca caggaaaact actcagcatg 3840
95 aactttgggg agccagagca gttttggcaa tccagggaag catgttgcca tctggtccct 3900
96 actgtagaaa tgtggtagaa ttctcagctc ctgagagggt gttctctgct tttgactcct 3960
97 gagctgggtt tgtagaaatg caggttggcg ttttttgtga agctaaggag ttttctgact 4020
98 ttaaccgggt cttatttgtt tagagtactc tgattattca ctttagtgat ttggagaatt 4080
99 cctattaaaa tcacatgaca tggaaaaaaa aaaaaaagg aat 4123
101 <210> SEQ ID NO: 2
102 <211> LENGTH: 507

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Input Set : A:\W122217.txt

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```

103 <212> TYPE: PRT
104 <213> ORGANISM: Artificial Sequence
106 <220> FEATURE:
107 <223> OTHER INFORMATION: Description of Artificial Sequence; Note =
108     synthetic construct
110 <400> SEQUENCE: 2
111 Met Gly Phe Phe Val Phe Ser Pro Thr Arg Tyr Leu Asp Gly Ile Ser
112 1      5      10      15
113 Gly Phe Phe Gln Trp Ala Phe Leu Leu Ser Leu Phe Leu Val Leu Phe
114      20      25      30
115 Lys Ala Val Gln Phe Tyr Leu Arg Arg Gln Trp Leu Leu Lys Thr Leu
116      35      40      45
117 Gln His Phe Pro Cys Met Pro Ser His Trp Leu Trp Gly His His Leu
118      50      55      60
119 Lys Asp Lys Glu Leu Gln Gln Ile Leu Ile Trp Val Glu Lys Phe Pro
120 65      70      75      80
121 Ser Ala Cys Leu Gln Cys Leu Ser Gly Ser Asn Ile Arg Val Leu Leu
122      85      90      95
123 Tyr Asp Pro Asp Tyr Val Lys Val Val Leu Gly Arg Ser Asp Pro Lys
124      100     105     110
125 Ala Ser Gly Ile Tyr Gln Phe Phe Ala Pro Trp Ile Gly Tyr Gly Leu
126      115     120     125
127 Leu Leu Leu Asn Gly Lys Lys Trp Phe Gln His Arg Arg Met Leu Thr
128      130     135     140
129 Pro Ala Phe His Tyr Asp Ile Leu Lys Pro Tyr Val Lys Ile Met Ala
130 145     150     155     160
131 Asp Ser Val Asn Ile Met Leu Asp Lys Trp Glu Lys Leu Asp Gly Gln
132      165     170     175
133 Asp His Pro Leu Glu Ile Phe His Cys Val Ser Leu Met Thr Leu Asp
134      180     185     190
135 Thr Val Met Lys Cys Ala Phe Ser Tyr Gln Gly Ser Val Gln Leu Asp
136      195     200     205
137 Glu Asn Ser Lys Leu Tyr Thr Lys Ala Val Glu Asp Leu Asn Asn Leu
138      210     215     220
139 Thr Phe Phe Arg Leu Arg Asn Ala Phe Tyr Lys Tyr Asn Ile Ile Tyr
140 225     230     235     240
141 Asn Met Ser Ser Asp Gly Arg Leu Ser His His Ala Cys Gln Ile Ala
142      245     250     255
143 His Glu His Thr Asp Gly Val Ile Lys Met Arg Lys Ser Gln Leu Gln
144      260     265     270
145 Asn Glu Glu Glu Leu Gln Lys Ala Arg Lys Lys Arg His Leu Asp Phe
146      275     280     285
147 Leu Asp Ile Leu Leu Phe Ala Arg Met Glu Asp Arg Asn Ser Leu Ser
148      290     295     300
149 Asp Glu Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe Glu Gly His
150 305     310     315     320
151 Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Phe Tyr Ala Leu Ala Thr
152      325     330     335
153 His Pro Glu His Gln Gln Arg Cys Arg Glu Glu Val Gln Ser Ile Leu

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```

154          340          345          350
155 Gly Asp Gly Thr Ser Val Thr Trp Asp His Leu Gly Gln Met Pro Tyr
156          355          360          365
157 Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Leu Tyr Pro Pro Val Ile
158          370          375          380
159 Ser Val Ser Arg Glu Leu Ser Ser Pro Val Thr Phe Pro Asp Gly Arg
160 385          390          395          400
161 Ser Ile Pro Lys Gly Ile Thr Ala Thr Ile Ser Ile Tyr Gly Leu His
162          405          410          415
163 His Asn Pro Arg Phe Trp Pro Asn Pro Lys Val Phe Asp Pro Ser Arg
164          420          425          430
165 Phe Ala Pro Asp Ser Ser His His Ser His Ala Tyr Leu Pro Phe Ser
166          435          440          445
167 Gly Gly Ser Arg Asn Cys Ile Gly Lys Gln Phe Ala Met Asn Glu Leu
168          450          455          460
169 Lys Val Ala Val Ala Leu Thr Leu Leu Arg Phe Glu Leu Leu Pro Asp
170 465          470          475          480
171 Pro Thr Arg Ile Pro Val Pro Ile Ala Arg Leu Val Leu Lys Ser Lys
172          485          490          495
173 Asn Gly Ile His Leu Cys Leu Lys Lys Leu Arg
174          500          505
176 <210> SEQ ID NO: 3
177 <211> LENGTH: 508
178 <212> TYPE: PRT
179 <213> ORGANISM: Artificial Sequence
181 <220> FEATURE:
182 <223> OTHER INFORMATION: Description of Artificial Sequence; Note =
183     synthetic construct
185 <400> SEQUENCE: 3
186 Met Ser Ala Ser Ala Leu Ser Ser Ile Arg Phe Pro Gly Ser Ile Ser
187 1          5          10          15
188 Glu Tyr Leu Gln Val Ala Ser Val Leu Ser Leu Leu Leu Leu Phe
189          20          25          30
190 Lys Thr Ala Gln Leu Tyr Leu His Arg Gln Trp Leu Leu Ser Ser Thr
191          35          40          45
192 Gln Gln Phe Pro Ser Pro Pro Ser His Trp Leu Phe Gly His Lys Ile
193          50          55          60
194 Leu Lys Asp Gln Asp Leu Gln Asp Ile Leu Thr Arg Ile Lys Asn Phe
195 65          70          75          80
196 Pro Ser Ala Cys Pro Gln Trp Leu Trp Gly Ser Lys Val Arg Ile Gln
197          85          90          95
198 Val Tyr Asp Pro Asp Tyr Met Lys Leu Ile Leu Gly Arg Ser Asp Pro
199          100          105          110
200 Lys Ala Asn Gly Ser Tyr Arg Phe Leu Ala Pro Trp Ile Gly Arg Gly
201          115          120          125
202 Leu Leu Met Leu Asp Gly Gln Thr Trp Phe Gln His Arg Arg Met Leu
203          130          135          140
204 Thr Pro Ala Phe His Tyr Asp Ile Leu Lys Pro Tyr Thr Glu Ile Met
205 145          150          155          160

```

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```

206 Ala Asp Ser Val Arg Val Met Leu Asp Lys Trp Glu Gln Ile Val Gly
207                               165                               170                               175
208 Gln Asp Ser Thr Leu Glu Ile Phe Arg His Ile Thr Leu Met Thr Leu
209                               180                               185                               190
210 Asp Thr Ile Met Lys Cys Ala Phe Ser His Glu Gly Ser Val Gln Leu
211                               195                               200                               205
212 Asp Arg Lys Tyr Lys Ser Tyr Ile Gln Ala Val Glu Asp Leu Asn Asp
213                               210                               215                               220
214 Leu Val Phe Ser Arg Val Arg Asn Ile Phe His Leu Asn Asp Ile Ile
215 225                               230                               235                               240
216 Tyr Arg Val Ser Ser Asn Gly Cys Lys Ala Asn Ser Ala Cys Gln Leu
217                               245                               250                               255
218 Ala His Asp His Thr Asp Gln Val Ile Lys Ser Arg Arg Ile Gln Leu
219                               260                               265                               270
220 Gln Asp Glu Glu Glu Leu Glu Lys Leu Lys Lys Arg Arg Leu Asp
221                               275                               280                               285
222 Phe Leu Asp Ile Leu Leu Phe Ala Arg Met Glu Asn Gly Lys Ser Leu
223                               290                               295                               300
224 Ser Asp Lys Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe Glu Gly
225 305                               310                               315                               320
226 His Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Phe Tyr Ala Leu Ala
227                               325                               330                               335
228 Thr Asn Pro Glu His Gln Gln Arg Cys Arg Lys Glu Ile Gln Ser Leu
229                               340                               345                               350
230 Leu Gly Asp Gly Thr Ser Ile Thr Trp Asn Asp Leu Asp Lys Met Pro
231                               355                               360                               365
232 Tyr Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Ile Tyr Pro Pro Val
233                               370                               375                               380
234 Pro Ser Val Ser Arg Glu Leu Ser Ser Pro Val Thr Phe Pro Asp Gly
235 385                               390                               395                               400
236 Arg Ser Leu Pro Lys Gly Ile His Val Met Leu Ser Phe Tyr Gly Leu
237                               405                               410                               415
238 His His Asn Pro Thr Val Trp Pro Asn Pro Glu Val Phe Asp Pro Ser
239                               420                               425                               430
240 Arg Phe Ala Pro Gly Ser Ser Arg His Ser His Ser Phe Leu Pro Phe
241                               435                               440                               445
242 Ser Gly Gly Ala Arg Asn Cys Ile Gly Lys Gln Phe Ala Met Asn Glu
243                               450                               455                               460
244 Leu Lys Val Ala Val Ala Leu Thr Leu Leu Arg Phe Glu Leu Leu Pro
245 465                               470                               475                               480
246 Asp Pro Thr Arg Val Pro Ile Pro Ile Pro Arg Ile Val Leu Lys Ser
247                               485                               490                               495
248 Lys Asn Gly Ile His Leu His Leu Lys Glu Leu Gln
249                               500                               505
251 <210> SEQ ID NO: 4
252 <211> LENGTH: 2116
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:

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→ Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\W122217.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:44 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:563 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:564 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:567 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:570 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:573 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:579 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:581 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:582 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:583 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:584 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:586 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:587 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:588 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:590 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:591 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:592 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:593 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:594 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:595 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:596 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:597 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:598 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:600 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:601 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:602 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:610 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

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L:611 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:613 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:614 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9